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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/054,967

DATE: 04/16/2002
TIME: 16:07:24

Input Set : N:\Crf3\RULE60\10054967.raw
Output Set: N:\CRF3\04162002\J054967.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: FREIDER, BRENT L.
 6 RUBEN, SIEVEN M.
 7 OLSEN, HENRIK S.
 8 RAGGIOLINI, MARCO
 10 (ii) TITLE OF INVENTION: CHEMOFINE -6
 12 (iii) NUMBER OF SEQUENCES 22
 14 (iv) CORRESPONDENCE ADDRESS:
 15 (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 16 B: STREET: 1100 NEW YORK AVENUE, SUITE 600
 17 C: CITY: WASHINGTON
 18 D: STATE: DC
 19 E: COUNTRY: USA
 20 F: ZIP: 20005-3944
 22 (v) COMPUTER READABLE FORM
 23 A: MEDIUM TYPE: Floppy disk
 24 B: COMPUTER: IBM PC compatible
 25 C: OPERATING SYSTEM: PC-DOS/MS-DOS
 26 D: SOFTWARE: PatentIn Release #1.0, Version #1.30
 28 (vi) CURRENT APPLICATION DATA:
 29 (A) APPLICATION NUMBER: US/10/054,967
 30 (B) FILING DATE: 25-Jan-2002
 31 (C) CLASSIFICATION
 33 (vii) PRIOR APPLICATION DATA
 35 (A) APPLICATION NUMBER: US/08/995,156
 36 (B) FILING DATE: Herewith
 38 (A) APPLICATION NUMBER: 60/042,269
 39 (B) FILING DATE: 1-MAR-1997
 41 (viii) ATTORNEY/AGENT INFORMATION:
 42 (A) NAME: STEFFE, ERIC K.
 43 (B) REGISTRATION NUMBER: 36,688
 44 (C) REFERENCE/DOCKET NUMBER: 1488,0340004
 46 (ix) TELECOMMUNICATION INFORMATION:
 47 (A) TELEPHONE: 202-371-2600
 48 (B) TELEFAX: 202-371-2546
 51 (2) INFORMATION FOR SEQ ID NO: 1:
 53 (i) SEQUENCE CHARACTERISTICS:
 54 (A) LENGTH: 300 base pairs
 55 (B) TYPE: nucleic acid
 56 (C) STRANNESS: single
 57 (D) POLARITY: linear
 58 (E) MOLTYPE: DNA (genomic)

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62     ix) FEATURE:
63         (A) NAME/KEY: CDS
64             B) LOCATION: 1..357
66     ix) FEATURE:
67         A) NAME/KEY: sig_peptide
68             B) LOCATION: 1..79
70     ix) FEATURE:
71         A) NAME/KEY: mat_peptide
72             B) LOCATION: 79..357
75     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
77 ATG GCA GGC CTG AIG ACC ATA GIA ACC AGC CII CTG IIC CII GGI GTC      48
78 Met Ala Gly Leu Met Thr Ile Val Thr Ser Leu Leu Phe Leu Gly Val
79 -26 -25           -20           -15
81 TGT CCC CAC CAC ATC ATC CCT ACG GGC TCT GTG GIC ATA CCC TCT CCC      96
82 Cys Ala His His Ile Ile Pro Thr Gly Ser Val Val Ile Pro Ser Pro
83 -10           -5           1           5
85 TGC TCC AIC ITC TTT GTI ICC AAG AGA AII CCI GAG AAC CGA GIG GTC      144
86 Cys Cys Met Phe Phe Val Ser Lys Arg Ile Pro Glu Asn Arg Val Val
87           10           15           20
89 AGC IAC CAG CTG ICC AGC AGG AGC ACA TGC CIC AAG GCA GGA GIG AIC      192
90 Ser Tyr Gln Leu Ser Ser Arg Ser Thr Cys Leu Lys Ala Gly Val Ile
91           25           30           35
93 ITC ACC ACC AAG AAC GGC CAG CAG ITC TGT GGC GAC CCC AAG CAG CAG      240
94 Phe Thr Thr Lys Lys Gly Gln Gln Phe Cys Gly Asp Pro Lys Gln Glu
95           40           45           50
97 TGG GTC CAG AGG TAC ATG AAG AAC CTG GAC GCC AAG CAG AAG AAG GCT      288
98 Trp Val Gln Arg Tyr Met Lys Asn Leu Asp Ala Lys Gln Lys Lys Ala
99 -55           60           65           70
101 TCC CCT AGG GCC AGG GCA GTG GCT GTC AAG GGC CCI GTC CAG AGA IAI      336
102 Ser Pro Arg Ala Arg Ala Val Ala Val Lys Gly Pro Val Gln Arg Tyr
103           75           80           85
105 CCT CGC AAU UAA ACC ACC TGC TAA      360
106 pro Gly Asn Gln Thr Thr Cys
107           90
112 (2) INFORMATION FOR SEQ ID NO: 2:
114     (i) SEQUENCE CHARACTERISTICS:
115         (A) LENGTH: 119 amino acids
116         (B) TYPE: amino acid
117         (D) TOPOLOGY: linear
119     (ii) MOLECULE TYPE: protein
121     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
123 Met Ala Gly Leu Met Thr Ile Val Thr Ser Leu Leu Phe Leu Gly Val
124 -26 -25           -20           -15
126 Cys Ala His His Ile Ile Pro Thr Gly Ser Val Val Ile Pro Ser Pro
127 -10           -5           1           5
129 Cys Cys Met Phe Phe Val Ser Lys Arg Ile Pro Glu Asn Arg Val Val
130           10           15           20
132 Ser Tyr Thr Leu Ser Ser Arg Ser Thr Lys Leu Lys Ala Gly Val Ile
133           25           30           35

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135 Phe Thr Thr Lys Lys Gly Cys Gln Phe Cys Gly Asp Pro Lys Gln Glu
 136 40 45 50
 138 Trp Val Gln Arg Tyr Met Lys Asn Leu Asp Ala Lys Gln Lys Lys Ala
 139 55 60 65 70
 141 Ser Pro Arg Ala Arg Ala Val Ala Val Lys Gly Pro Val Gln Arg Tyr
 142 75 80 85
 144 Pro Gly Asn Gln Thr Thr Cys
 145 90

147 (2) INFORMATION FOR SEQ ID NO: 3:

149 (i) SEQUENCE CHARACTERISTICS:
 150 A LENGTH: 26 base pairs
 151 B TYPE: nucleic acid
 152 C STRANDEDNESS: double
 153 D TOPOLOGY: linear

155 (ii) MOLECULE TYPE: DNA (genomic)

160 (xi) SEQUENCE DESCRIPTION: SEQ ID NO 3:

162 TCAGGAICCC CTACGGGCIC GTGGTC 26

164 (2) INFORMATION FOR SEQ ID NO 4:

166 (i) SEQUENCE CHARACTERISTICS:
 167 A LENGTH: 26 base pairs
 168 B TYPE: nucleic acid
 169 C STRANDEDNESS: double
 170 D TOPOLOGY: linear

172 (ii) MOLECULE TYPE: DNA (genomic)

177 (xi) SEQUENCE DESCRIPTION: SEQ ID NO 4:

179 AGACCGGGCAC CAAAAIGAGA TCTCGC 26

181 (2) INFORMATION FOR SEQ ID NO: 5:

183 (i) SEQUENCE CHARACTERISTICS:
 184 A LENGTH: 99 amino acids
 185 B TYPE: amino acid
 186 C TOPOLOGY: linear
 188 (ii) MOLECULE TYPE: protein

193 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

195 Met Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Leu Ile Ala Ala Thr
 196 1 5 10 15
 197 Phe Ile Pro Gln Gly Leu Ala Gln Pro Asp Ala Ile Asn Ala Pro Val
 198 20 25 30
 201 Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu
 202 35 40 45
 204 Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val
 205 50 55 60
 207 Ile Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln
 208 65 70 75 80
 210 Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr
 211 85 90 95

213 Pro Lys Thr

217 (2) INFORMATION FOR SEQ ID NO: 6:

219 (i) SEQUENCE CHARACTERISTICS:
 220 (ii) LENGTH: 285 base pairs

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221 (B) TYPE: nucleic acid
 222 (C) STRANDEDNESS: double
 223 (D) TOPOLOGY: linear
 225 (ii) MOLECULE TYPE: cDNA
 226 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 227 ACGGTGGTCA TACCTTCGCC GIGGCGCATG TTCTTGTGTA GCAAGCCAT TCCCTGAAAAC 60
 228 CGTGTGGTCA GCTACCAGCT GTCCAGCGGC AGCACCTGCC TGAAAGCGG CGTGATCTTC 120
 229 ACCACCAAAA AGGGCCAGCA GCTCTGGGC GACCCGAAAC AACAGTGCGT CCAGCGIIAC 180
 230 ATGAAAAAACC TGGACGCCAA ACAGAAGAAA CCTCTCCCTC CIGCCCCGGC AGGGCTGTC 240
 231 AAAGGUCCIG TTCAGCGTIA TCGGGGCAAC CAAACCACCT GTCAA 285
 242 (2) INFORMATION FOR SEQ ID NO: 7:
 243 (i) SEQUENCE CHARACTERISTICS:
 244 (A) LENGTH: 96 base pairs
 245 (B) TYPE: nucleic acid
 246 (C) STRANDEDNESS: single
 247 (D) TOPOLOGY: linear
 248 (ii) MOLECULE TYPE: cDNA
 249 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 250 GACICCATGG TGTTATACC TTCTCCGTGC ICCATGTCT TTGTTAGCAA GCGCATTCCI 60
 251 GAAAACCGTG TGTTAGCTA CCAGUTGTCC AGCCGC 96
 261 (2) INFORMATION FOR SEQ ID NO: 8:
 262 (i) SEQUENCE CHARACTERISTICS:
 263 (A) LENGTH: 97 base pairs
 264 (B) TYPE: nucleic acid
 265 (C) STRANDEDNESS: single
 266 (D) TOPOLOGY: linear
 267 (ii) MOLECULE TYPE: cDNA
 268 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 269 GTTTCCGGGIC GCCACAGAAC TGCTGGCCCT TTIIIGGTGGT GAAGATCAGG CCAGCTTICA 60
 270 GGCAGGTGCT GGGCTGGAC AGCCTGGTAC TGACCCAC 97
 280 (2) INFORMATION FOR SEQ ID NO: 9:
 281 (i) SEQUENCE CHARACTERISTICS:
 282 (A) LENGTH: 98 base pairs
 283 (B) TYPE: nucleic acid
 284 (C) STRANDEDNESS: single
 285 (D) TOPOLOGY: linear
 286 (ii) MOLECULE TYPE: cDNA
 287 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 288 AAGGUCCAGC AGTCTCTGCG CGAATGGAAA CAAGAGTGGG TCCAGGGTTA CATGAAAAAC 61
 289 CTGGACGCCA AACAGAAGAA AGCTTCCCT CGGCCCG 98
 299 (2) INFORMATION FOR SEQ ID NO: 10:
 300 (i) SEQUENCE CHARACTERISTICS:
 301 (A) LENGTH: 99 base pairs
 302 (B) TYPE: nucleic acid
 303 (C) STRANDEDNESS: single
 304 (D) TOPOLOGY: linear
 305 (ii) MOLECULE TYPE: cDNA
 306 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 307 ATGAAATTC TAAAGAAGCG GTCCTGGTCTGAGATAGG TGAAGAAGG TGTGGGACAG 62

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Input Set : N:\Crf3\RULE60\10054967.raw
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316	CCACGCGCG GGCACGGAGGG GAAGCTTCTT TGTGTTGG	99
318	(2) INFORMATION FOR SEQ ID NO: 11:	
320	(i) SEQUENCE CHARACTERISTICS:	
321	(A) LENGTH: 34 base pairs	
322	(B) TYPE: nucleic acid	
323	(C) STRANDEDNESS: single	
324	(D) TOPOLOGY: linear	
326	(ii) MOLECULE TYPE: cDNA	
331	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:	
333	GACGGATCCC CATACTGGG TTAACTTC TCCTG	34
335	(2) INFORMATION FOR SEQ ID NO: 12:	
337	(i) SEQUENCE CHARACTERISTICS:	
338	(A) LENGTH: 32 base pairs	
339	(B) TYPE: nucleic acid	
340	(C) STRANDEDNESS: single	
341	(D) TOPOLOGY: linear	
343	(ii) MOLECULE TYPE: cDNA	
348	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:	
350	GACTGGTACC TTAGCAGGTG GTTGGTTGC CC	32
352	(2) INFORMATION FOR SEQ ID NO: 13:	
354	(i) SEQUENCE CHARACTERISTICS:	
355	(A) LENGTH: 36 base pairs	
356	(B) TYPE: nucleic acid	
357	(C) STRANDEDNESS: single	
358	(D) TOPOLOGY: linear	
360	(ii) MOLECULE TYPE: cDNA	
365	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:	
367	GACTGGTACC TTATCAACGA CGGGAAAGCTT TCTTCT	36
369	(2) INFORMATION FOR SEQ ID NO: 14:	
371	(i) SEQUENCE CHARACTERISTICS:	
372	(A) LENGTH: 37 base pairs	
373	(B) TYPE: nucleic acid	
374	(C) STRANDEDNESS: single	
375	(D) TOPOLOGY: linear	
377	(ii) MOLECULE TYPE: cDNA	
382	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:	
384	CAATGGTACG CTATCAAGCC ACIGGCGCGG CAGGAG	37
386	(2) INFORMATION FOR SEQ ID NO: 15:	
388	(i) SEQUENCE CHARACTERISTICS:	
389	(A) LENGTH: 34 base pairs	
390	(B) TYPE: nucleic acid	
391	(C) STRANDEDNESS: single	
392	(D) TOPOLOGY: linear	
394	(ii) MOLECULE TYPE: cDNA	
399	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:	
401	GAATTAATG GTTAAATT CTCGGGGGGG CAAG	34
403	(2) INFORMATION FOR SEQ ID NO: 16:	
405	(i) SEQUENCE CHARACTERISTICS:	
406	(A) LENGTH: 31 base pairs	

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/054,967

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Input Set : N:\Crf3\RULE60\10054967.raw

Output Set: N:\CRF3\04162002\J054967.raw

L:29 M:229 C: Keyword misspelled or invalid format. [(A) APPLICATION NUMBER:]

L:30 M:229 C: Keyword misspelled or invalid format. [(B) FILING DATE:]